

IN THE SPECIFICATION

Please amend the specification by replacing the paragraph on page 17, line 26, - page 18, line as follows:

For the alignments presented herein (see, Figures 3A and 3B) for the AAV serotype, the CLUSTALW program was employed with parameters set as follows: scoring matrix BLOSUM, gap open 10, gap extend 0.1, gap distance 40% and transitions/transversions 0.5; specific 1residue penalties for hydrophobic amino acids (~~DEGKNPQRS~~) (D, E, G, K, N, P, Q, R and S), distance between gaps for which the penalties are augmented was 8, and gaps of ~~extemities~~ extremities penalized less than internal gaps